This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claims 1-70 (canceled)

Claim 71 (original): A centromere nucleic acid sequence prepared by the method of claim 1.

Claim 72 (original): A non-human organism prepared by the method of claim 56.

Claim 73 (original): A progeny of any generation of the organism of claim 72, said organism comprising said first methylated nucleic acid segment.

Claim 74 (original): A method of obtaining a centromere nucleic acid sequence from a selected organism comprising the steps of

a) preparing a first sample of genomic DNA from a selected organism;

b) contacting said genomic DNA with a strand-specific methylation sensitive restriction endonuclease;

c) nick-translating the genomic DNA; and

c) detecting a centromere nucleic acid sequence that hybridizes to the nick-translated genomic DNA.

75. (original): The method of claim 74, wherein the strand-specific methylation sensitive restriction endonuclease is selected from the group consisting of HpaI, KpnI, MaeII, or Sau3A I.

76. (original): The method of claim 74, wherein detecting comprises screening an array.

77. (original): The method of claim 76, wherein said screening comprises the steps of

a) obtaining an array comprising cloned genomic DNA from said selected organism; and

b) detecting a centromere nucleic acid sequence from said cloned genomic DNA of said array by hybridizing the nick translated genomic DNA to said array.

78. (original): The method of claim 77, wherein a plurality of centromere nucleic acid sequences are detected from said array.

79. (original): The method of claim 77, wherein said array comprises said cloned genomic DNA attached to a solid support.

80. (original): The method of claim 79, wherein said array is further defined as comprising cloned genomic DNA attached to said solid support in a selected pattern

81. (original): The method of claim 80, wherein said selected pattern comprises a grid.

82. (original): The method of claim 79, wherein said cloned genomic DNA comprises DNA cloned in a bacterial artificial chromosome.

83. (original): The method of claim 79, wherein said cloned genomic DNA comprises DNA cloned in a yeast artificial chromosome.

84. (original): The method of claim 79, wherein the solid support comprises a microscope slide.

85. (original): The method of claim 79, wherein said solid support comprises a hybridization filter.

86. (original): The method of claim 77, wherein said array comprises a plurality of DNA pools, said pools comprising the nucleic acid sequences of at least a first and a second clone comprising genomic DNA from said selected organism.

87. (original): The method of claim 74, wherein said contacting is further defined as comprising:

a) obtaining a second sample of genomic DNA from said selected organism;

b) contacting said second sample of genomic DNA with an isoschizomer of said strand-specific methylation sensitive restriction endonuclease, wherein said isoschizomer is not a strand-specific methylation sensitive restriction endonuclease;

c) resolving separately said first and said second samples of genomic DNA following said contacting; and

d) selecting a plurality of hemimethylated nucleic acid segments from at least a first nucleic acid fraction present in said first sample of genomic DNA and not present in said second sample of genomic DNA.

88. (original): The method of claim 74, wherein said nick-translating comprises radioactively labeling the genomic DNA.

89. (original): The method of claim 74, wherein said nick-translating comprises labeling the genomic DNA with an antigen.

90. (original): The method of claim 74, wherein said nick-translating comprises labeling the genomic DNA with a fluorophore.

91. (original): The method of claim 74, wherein said selected organism is a plant.

92. (original): The method of claim 91, wherein said plant is a dicotyledonous plant.

93. (original): The method of claim 92, wherein said dicotyledonous plant is selected from the group consisting of tobacco, tomato, potato, sugar beet, pea, carrot, cauliflower, broccoli, soybean, canola, sunflower, alfalfa, cotton and Arabidopsis.

94. (original): The method of claim 93, wherein said dicotyledonous plant is Arabidopsis thaliana.

95. (original): The method of claim 91, wherein said plant is a monocotyledonous plant.

96. (original): The method of claim 95, wherein said monocotyledonous plant is selected from the group consisting of wheat, maize, rye, rice, turfgrass, oat, barley, sorghum, millet, and sugarcane.

97. (original): The method of claim 96, wherein said monocotyledonous plant is maize.

98. (original): The method of claim 74, wherein said selected organism is a mammal.

99. (original): The method of claim 74, wherein said selected organism is a human.

100. (original): The method of claim 74, further defined as comprising fluorescent in situ hybridization of the centromere nucleic acid sequence.

101. (original): The method of claim 74, further defined as comprising determining the nucleic acid sequence of the centromere nucleic acid sequence.

102. (original): The method of claim 101, further defined as comprising comparing the nucleic acid sequence of the centromere nucleic acid sequence to a known centromere sequence.

103. (original): The method of claim 74, further defined as comprising transforming a cell with the centromere nucleic acid sequence.

104. (original): The method of claim 103, wherein said cell is further defined as integratively transformed with said centromere nucleic acid sequence.

105. (original): The method of claim 103, wherein said cell is further defined as non-integratively transformed with said centromere nucleic acid sequence.

106. (original): The method of claim 104, further comprising screening for a phenotypic effect present in the integratively transformed cells or an organism comprising the cells, wherein said phenotypic effect is absent in a control cell not integratively transformed with said centromere nucleic acid sequence or an organism comprising said control cell.

107. (original): The method of claim 106, wherein said phenotypic effect is selected from the group consisting of reduced viability, reduced efficiency of said transforming, genetic instability in the integratively transformed nucleic acid, aberrant tissue sectors, increased ploidy, aneuploidy, and increased integrative transformation in distal or centromeric chromosome regions.

108. (original): The method of claim 103, wherein said centromere nucleic acid sequence is further defined as comprising a recombinant construct.

109. (original): The method of claim 103, wherein said centromere nucleic acid sequence is further defined as comprising cloned DNA.

110. (original): The method of claim 109, wherein the cloned DNA is not methylated.

111. (original): The method of claim 109, wherein the cloned DNA is remethylated prior to said transforming.

112. (original): The method of claim 111, wherein the remethylated DNA is hemimethylated.

113. (original): The method of claim 108, wherein said recombinant construct comprises a telomere.

114. (original): The method of claim 108, wherein said recombinant construct comprises an autonomous replicating sequence (ARS).

115. (original): The method of claim 108, wherein said recombinant construct comprises a structural gene.

116. (original): The method of claim 115, wherein said structural gene comprises a selectable or screenable marker gene.

117. (original): A centromere nucleic acid sequence prepared by the method of claim 74.

118. (original): A non-human organism prepared by the method of claim 103.

119. (original): A progeny of any generation of the organism of claim 118, said organism comprising said first methylated nucleic acid segment.